## SECUENCE LISTING

```
<110> Allen, Keith D.
Matthews, William
Moore, Mark
```

<120> TRANSGENIC MICE CONTAINING ADRENOCORTICOTROPIN HORMONE RECEPTOR GENE DISRUPTIONS

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<130> R-605
<140> To Be Assigned
<141> Herewith
<150> US 60/254,906
<151> 2000-12-11
<150> US 60/324,583
<151> 2001-09-24
<160> 4
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 1100
<212> DNA
<213> Mus musculus
<400> 1
atttatttat ttaatcatot catatgtgto tatgtg
caccaaagaa aacatactgc agaaacaatc gtgatt
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atttatttat ttaatcatct catatgtgtc tatgtgttct gtttaacctc agatccttcc 60 acacaaagaa aacatactgc agaaacaatc gtgatttctg taagtcaacg gcaaacacca 120 ccccgtctt aacggccagc aggaaaaaat gaagcatatt atcaattcgt atgaacacac 180 caatgacacc gcaagaaata actccgattg tcctgatgta gttttgccag aagagatatt 240 tttcacaatc tctgtcattg gcatattgga gaacttgatt gtcctcctgg ctgtgatcaa 300 aaataaaaat ctccagtccc ccatgtattt tttcatctgc agtttggcca tttctgacat 360 gttgggcagt ctgtataaga tcttggaaaa catcctgatc atgttcagaa acatgggtta 420 tettaageet egtggeagtt ttgaaageac ageagatgae ateattgaet geatgtteat 480 cetetetttg etgggeteta tetteageet gtetgteatt geagetgace gttacateae 540 catcttccat gccctgcaat accatagcat tgtgaccatg cgccgcacca tcatcaccct 600 aacaattato tggatgttot goacagggag oggoatoaco atggtgatot totoccacca 660 catececaca gtgeteacet teacateget gtteeetttg atgetggttt ttateetgtg 720 tetetacate caeatgttet taettgeeeg eteccatget aggaagatet etaccettee 780 tagaaccaac atgaagggtg ccatgacact aaccatcctt cttggagtct tcatcttctg 840 ttgggccccc tttgtgctcc atgttctctt aatgaccttc tgcccaaata acccttactg 900 tgtttgctac atgtctctct tccaggtcaa tggcatgttg atcatgtgca atgcagttat 960 tgaccccttt atatatgcct ttcggagccc agagctcaga gatgcattca aaaggatgct 1020 cttctgcaac cggtattagt agaatttttg atccctgctt tgagtgttgt aaagggacca 1080 aataacacat cagtctgaca

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<210> 2
<211> 296
<212> PRT
<213> Mus musculus
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<400> 2
Met Lys His Ile Ile Asn Ser Tyr Glu His Thr Asn Asp Thr Ala Arg
1 5 10
15 Asn Asn Ser Asp Cys Pro Aso Val Val Leu Pro Glu Glu Tle Phe Phe

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25
Thr Ile Ser Val Ile Gly Ile Leu Glu Asn Leu Ile Val Leu Leu Ala
                            40
                                                45
Val Ile Lys Asn Lys Asn Leu Gln Ser Pro Met Tyr Phe Phe Ile Cys
                        55
                                            60
Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Leu Tyr Lys Ile Leu Glu
                    70
                                        75
Asn Ile Leu Ile Met Phe Arg Asn Met Gly Tyr Leu Lys Pro Arg Gly
                                                        95
                85
                                    90
Ser Phe Glu Ser Thr Ala Asp Asp Ile Ile Asp Cys Met Phe Ile Leu
                                                    110
            100
                                105
Ser Leu Leu Gly Ser Ile Phe Ser Leu Ser Val Ile Ala Ala Asp Arg
                            120
Tyr Ile Thr Ile Phe His Ala Leu Gln Tyr His Ser Ile Val Thr Met
                        135
                                            140
Arg Arg Thr Ile Ile Thr Leu Thr Ile Ile Trp Met Phe Cys Thr Gly
145
                    150
                                        155
Ser Gly Ile Thr Met Val Ile Phe Ser His His Ile Pro Thr Val Leu
                165
                                    170
                                                        175
Thr Phe Thr Ser Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu
            180
                                185
Tyr Ile His Met Phe Leu Leu Ala Arg Ser His Ala Arg Lys Ile Ser
        195
                            200
                                                205
Thr Leu Pro Arg Thr Asn Met Lys Gly Ala Met Thr Leu Thr Ile Leu
   210
                        215
                                            220
Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val Leu His Val Leu
225
                    230
                                        235
Leu Met Thr Phe Cys Pro Asn Asn Pro Tyr Cys Val Cys Tyr Met Ser
                245
                                    250
Leu Phe Gln Val Asn Gly Met Leu Ile Met Cys Asn Ala Val Ile Asp
            260
                                265
                                                    270
Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg Asp Ala Phe Lys
        275
                            280
Arg Met Leu Phe Cys Asn Arg Tyr
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<210> 3
<211> 200
<212> DNA
<213> Artificial Sequence
<220>
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290

<223> Targeting Vector

<400> 3
atgaacaca caatgacace gcaagaaata acteegattg teetgatgta gttttgecag 60
aagagatatt tttcacaate teetgteattg gcatattgga gaacttgatt gteeteetgg 120
ctgtgateaa aaataaaaat eteeagteee coatgtattt tttcateege agtttggeca 180
tttctgaact gttgggeagt
200

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<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence
<220>
<223> Targeting Vector
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<400> 4
ggtgccatga cactaaccat ccttcttgga gtcttcatct tctgttgggc cccctttgtg 60

ctccatgttc tcttaatgac tttctgccca aataaccett actgtgtttg ctacatgtct 120 ctcttccagg tcaatggcat gttgatcatg tgcaatgcag ttattgaccc ctttatatat 180 gcctttcgga gcccagaggt 200